

## SEQUENCE LISTING

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				-				gac Asp								163
								tcc Ser 30								211
gac Asp			_					ttc Phe				-				259
ata Ile								gct Ala								307
tcc Ser 70			_					aac Asn				_	_	_		355
caa Gln																403

gta gtt cca ctc ggc aaa cta aaa gga atc aaa ttc atg agc ata ttc Val Val Pro Leu Gly Lys Leu Lys Gly Ile Lys Phe Met Ser Ile Phe

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105	110	115

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_		caa Gln		-			_			_	_			-		547
		cga Arg			_											595
		tca Ser														643
_	_	ggt Gly														691
		cat His 200		_		_			_				_	_	-	739
	_	atc Ile			_					_			_	_		787
		cct Pro														835
		ttg Leu	_	_					-							883
		gat Asp														931
		tcc Ser 280				_	_	_	-	-	_	_			_	979
	_	acc Thr		_		-		_		_	_		-			1027
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		ggt Gly														1123
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		agg Arg 360														1219
		gtg Val														1267
		att Ile														1315
		atg Met														1363
		gtt Val														1411
_		ggt Gly 440		_	_			-	_	_				_		1459
		tca Ser	_	_								-		_	_	1507
		cat His														1555
		cgc Arg	_		_	_			-		_				-	1603
		ggt Gly							_		_	_		_	-	1651
		agt Ser 520														1699
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		ggc Gly					-	-	-	_	_					1795
	_	ttg Leu					_	_		_				_	_	1843
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gag gca cgg cga aac aag agt gta tct gaa ttt tca cgc gcg gtg aca Glu Ala Arg Arg Asn Lys Ser Val Ser Glu Phe Ser Arg Ala Val Thr 630 635 640 645	035
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atg agc acc aaa ggt gtg gat ttt ttt gct gtg tat ttt ttc aag gag 2:  Met Ser Thr Lys Gly Val Asp Phe Phe Ala Val Tyr Phe Phe Lys Glu 665 670 675	131
aag aaa ttg agg ctc atg aag tgt tct gat aga ttg aaa gtt tcg ctt 2: Lys Lys Leu Arg Leu Met Lys Cys Ser Asp Arg Leu Lys Val Ser Leu 680 685 690	179
gag cca ttt agt ttt gag cta atg aca gtg tct cca gtg aaa gtg ttt 2: Glu Pro Phe Ser Phe Glu Leu Met Thr Val Ser Pro Val Lys Val Phe 695 700 705	227
tcg aaa agg ttt ata cag ttt gca ccg att ggg tta gtg aac atg ctg Ser Lys Arg Phe Ile Gln Phe Ala Pro Ile Gly Leu Val Asn Met Leu 710 725	275
aac tct ggt ggt gcg att cag tct ctg gag ttt gat gat aat gca agt 2: Asn Ser Gly Gly Ala Ile Gln Ser Leu Glu Phe Asp Asp Asn Ala Ser 730 735 740	323
ttg gtc aag att ggg gtg aga ggt tgc ggg gag atg agc gtg ttt gcg 2. Leu Val Lys Ile Gly Val Arg Gly Cys Gly Glu Met Ser Val Phe Ala 745 750 755	371
tct gag aaa ccg gtt tgc tgc aaa att gat ggg gtt aag gtg aaa ttt 29 Ser Glu Lys Pro Val Cys Cys Lys Ile Asp Gly Val Lys Val Lys Phe 760 765 770	419
ctt tat gag gac aaa atg gca aga gtt caa att ctg tgg cct agt tct 24 Leu Tyr Glu Asp Lys Met Ala Arg Val Gln Ile Leu Trp Pro Ser Ser 775 780 785	467
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Asp Asp Ser Gly Met Asn Arg Thr Ser Ala Gly Glu Gln Met Pro Cys

290	295	300
200	233	300

Arg 305	Leu	Val	Lys	Tyr	Glu 310	Glu	Asn	Ser	Lys	Phe 315	Arg	Glu	Tyr	Glu	Asn 320
Pro	Glu	Asn	Gly	Gly 325	Lys	Lys	Gly	Leu	Gly 330	Gly	Phe	Val	Arg	Asp 335	Leu
Lys	Glu	Glu	Phe 340	Gly	Ser	Val	Glu	Ser 345	Val	Tyr	Val	Trp	His 350	Ala	Leu
Cys	Gly	Tyr 355	Trp	Gly	Gly	Val	Arg 360	Pro	Gly	Val	His	Gly 365	Met	Pro	Lys
Ala	Arg 370	Val	Val	Val	Pro	Lys 375	Val	Ser	Gln	Gly	Leu 380	Lys	Met	Thr	Met
Glu 385	Asp	Leu	Ala	Val	Asp 390	Lys	Ile	Val	Glu	Asn 395	Gly	Val	Gly	Leu	Val 400
Pro	Pro	Asp	Phe	Ala 405	His	Glu	Met	Phe	Asp 410	Gly	Leu	His	Ser	His 415	Leu
Glu	Ser	Ala	Gly 420	Ile	Asp	Gly	Val	Lys 425	Val	Asp	Val	Ile	His 430	Leu	Leu
Glu	Leu	Leu 435	Ser	Glu	Glu	Tyr	Gly 440	Gly	Arg	Val	Glu	Leu 445	Ala	Arg	Ala
Tyr	Tyr 450	Lys	Ala	Leu	Thr	Ser 455	Ser	Val	Lys	Lys	His 460	Phe	Lys	Gly	Asn
Gly 465	Val	Ile	Ala	Ser	Met 470	Glu	His	Cys	Asn	Asp 475	Phe	Phe	Leu	Leu	Gly 480
Thr	Glu	Ala	Ile	Ser 485	Leu	Gly	Arg	Val	Gly 490	Asp	Asp	Phe	Trp	Cys 495	Ser
Asp	Pro	Ser	Gly 500	Asp	Pro	Asn	Gly	Thr 505	Tyr	Trp	Leu	Gln	Gly 510	Cys	His
Met	Val	His 515	Cys	Ala	Tyr	Asn	Ser 520	Leu	Trp	Met	Gly	Asn 525	Phe	Ile	Gln
Pro	Asp 530	Trp	Asp	Met	Phe	Gln 535	Ser	Thr	His	Pro	Cys 540	Ala	Glu	Phe	His
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					330					JJJ					
Val	Gly	Asn	His	Asn 565		Lys	Leu	Leu	Lys 570		Leu	Val	Leu	Pro 575	Asp
	Gly Ser			565	Phe				570	Ser				575	
Gly	_	Ile	Leu 580	565 Arg	Phe Cys	Gln	His	Tyr 585	570 Ala	Ser Leu	Pro	Thr	Arg 590	575 Asp	Cys

Gly 625	Gly	Trp	Суѕ	Pro	Glu 630	Ala	Arg	Arg	Asn	Lys 635	Ser	Val	Ser	Glu	Phe 640	
Ser	Arg	Ala	Val	Thr 645	Cys	Tyr	Ala	Ser	Pro 650	Glu	Asp	Ile	Glu	Trp 655	Cys	
Asn	Gly	Lys	Thr 660	Pro	Met	Ser	Thr	Lys 665	Gly	Val	Asp	Phe	Phe 670	Ala	Val	
Tyr	Phe	Phe 675	Lys	Glu	Lys	Lys	Leu 680	Arg	Leu	Met	Lys	Cys 685	Ser	Asp	Arg	
Leu	Lys 690	Val	Ser	Leu	Glu	Pro 695	Phe	Ser	Phe	Glu	Leu 700	Met	Thr	Val	Ser	
Pro 705	Val	Lys	Val	Phe	Ser 710	Lys	Arg	Phe	Ile	Gln 715	Phe	Ala	Pro	Ile	Gly 720	
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Asp	Asp	Asn	Ala 740	Ser	Leu	Val	Lys	Ile 745	Gly	Val	Arg	Gly	Cys 750	Gly	Glu	
Met	Ser	Val 755	Phe	Ala	Ser	Glu	Lys 760	Pro	Val	Cys	Cys	Lys 765	Ile	Asp	Gly	
Val	Lys 770	Val	Lys	Phe	Leu	Tyr 775	Glu	Asp	Lys	Met	Ala 780	Arg	Val	Gln	Ile	
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_	aac Asn			_		_					_					157
	gcc Ala															205
	acc Thr															253

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-	gac Asp	_	-	 _		 			

					ggc Gly					301
					aag Lys					349
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					ccc Pro					541
					cgt Arg					589
					cat His 185					637
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 					ata Ile	_	-		 _	733
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					aag Lys					973

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		_	_	atc Ile	_	_			-		_				1213
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				ggt Gly											1693

_	cac His			_	_		_	_		_	_		_		_	1741
	ttg Leu						-				_		_	-		1789
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	aaa Lys										_					1885
	tgt Cys 610															1933
	gtg Val															1981
	agc Ser															2029
	aag Lys	_				_		_	_	_				_	_	2077
	tca Ser									_						2125
	gtg Val 690															2173
	atg Met															2221
cac His	ata Ile	gat Asp	gtg Val	gtc Val 725	aaa Lys	att Ile	ggg Gly	gtt Val	agg Arg 730	ggt Gly	tgt Cys	ggg Gly	gag Glu	atg Met 735	aag Lys	2269
	ttt Phe															2317
	aaa Lys															2365
	agt Ser 770												tgat	ccct	.ga	2414

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Leu Ala Asn Gly His Pro Phe Leu Thr Glu Val Pro Glu Asn Ile Ile  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Val Thr Pro Ser Pro Ile Asp Ala Lys Ser Ser Lys Asn Asn Glu Asp 50 55 60

Asp Asp Val Val Gly Cys Phe Val Gly Phe His Ala Asp Glu Pro Arg 65 70 75 80

Ser Arg His Val Ala Ser Leu Gly Lys Leu Arg Gly Ile Lys Phe Met 85 90 95

Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr His Trp Val Gly Ser 100 105 110

Asn Gly His Glu Leu Glu His Glu Thr Gln Met Met Leu Leu Asp Lys 115 120 125

Asn Asp Gln Leu Gly Arg Pro Phe Val Leu Ile Leu Pro Ile Leu Gln 130 135 140

Ala Ser Phe Arg Ala Ser Leu Gln Pro Gly Leu Asp Asp Tyr Val Asp 145 150 155 160

Val Cys Met Glu Ser Gly Ser Thr Arg Val Cys Gly Ser Ser Phe Gly 165 170 175

Ser Cys Leu Tyr Val His Val Gly His Asp Pro Tyr Gln Leu Leu Arg 180 185 190

Glu Ala Thr Lys Val Val Arg Met His Leu Gly Thr Phe Lys Leu Leu 195 200 205

Glu Glu Lys Thr Ala Pro Val Ile Ile Asp Lys Phe Gly Trp Cys Thr 210 220

Trp Asp Ala Phe Tyr Leu Lys Val His Pro Ser Gly Val Trp Glu Gly 225 230 235 240

Val Lys Gly Leu Val Glu Gly Gly Cys Pro Pro Gly Met Val Leu Ile 245 250 255

Asp Asp Gly Trp Gln Ala Ile Cys His Asp Glu Asp Pro Ile Thr Asp 260 265 270

Gln	Glu	Gly 275	Met	Lys	Arg	Thr	Ser 280	Ala	Gly	Glu	Gln	Met 285	Pro	Cys	Arg
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Gln	Phe	Arg	Ser	Val 325	Glu	Gln	Val	Tyr	Val 330	Trp	His	Ala	Leu	Cys 335	Gly
Tyr	Trp	Gly	Gly 340	Val	Arg	Pro	Lys	Val 345	Pro	Gly	Met	Pro	Gln 350	Ala	Lys
Val	Val	Thr 355	Pro	Lys	Leu	Ser	Asn 360	Gly	Leu	Lys	Leu	Thr 365	Met	Lys	Asp
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Ala	Gly	Ile	Asp	Gly 405	Val	Lys	Val	Asp	Val 410	Ile	His	Leu	Leu	Glu 415	Met
Leu	Ser	Glu	Glu 420	Tyr	Gly	Gly	Arg	Val 425	Glu	Leu	Ala	Lys	Ala 430	Tyr	Tyr
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Ile	Ala 450	Ser	Met	Glu	His	Cys 455	Asn	Asp	Phe	Phe	Leu 460	Leu	Gly	Thr	Glu
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His	Cys	Ala	Tyr 500	Asn	Ser	Leu	Trp	Met 505	Gly	Asn ·	Phe	Ile	Gln 510	Pro	Asp
Trp	Asp	Met 515	Phe	Gln	Ser	Thr	His 520	Pro	Cys	Ala	Glu	Phe 525	His	Ala	Ala
Ser	Arg 530	Ala	Ile	Ser	Gly	Gly 535	Pro	Val	Tyr	Val	Ser 540	Asp	Суѕ	Val	Gly
Lys 545	His	Asn	Phe	Lys	Leu 550	Leu	Lys	Ser	Leu	Ala 555	Leu	Pro	Asp	Gly	Thr 560
Ile	Leu	Arg	Cys	Gln 565	His	Tyr	Ala	Leu	Pro 570	Thr	Arg	Asp	Cys	Leu 575	Phe
Glu	Asp	Pro	Leu 580	His	Asp	Gly	Lys	Thr 585	Met	Leu	Lys	Ile	Trp 590	Asn	Leu
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Trp Cys Pro Va	al Thr Arg Arg 615		Ala Ser Glu 620	Phe Ser Gln
Thr Val Thr Cy 625	vs Leu Ala Ser 630	Pro Gln Asp	Ile Glu Trp 635	Ser Asn Gly 640
Lys Ser Pro I	e Cys Ile Lys 645	Gly Met Asn 650		Val Tyr Leu 655
Phe Lys Asp Hi 66		Leu Met Lys 665		Lys Leu Glu 670
Val Ser Leu Gl 675	u Pro Phe Thr	Phe Glu Leu 680	Leu Thr Val	Ser Pro Val
Ile Val Leu Se 690	r Lys Lys Leu 695		Ala Pro Ile 700	Gly Leu Val
Asn Met Leu As 705	n Thr Gly Gly 710	Ala Ile Gln	Ser Met Glu 715	Phe Asp Asn 720
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Val Phe Ala Se		Val Ser Cys 745		Gly Val Val 750
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											ccc Pro					529
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											ttt Phe					625
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											ccg Pro					721
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											ggc Gly					817
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											gtc Val 300					913

	atg Met															961
	tac Tyr	_	_			-		-								1009
	gtc Val															1057
	gag Glu															1105
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	gtg Val															1201
	gat Asp															1249
	gcc Ala															1297
	gga Gly															1345
	tcc Ser 450			_	_	-					_		_	_	_	1393
	ttt Phe															1441
	tat Tyr		_				-	_					_			1489
	ggg Gly															1537
	cac His															1585
	gga Gly 530															1633
tac	cta	ttc	cac	gag	aag	aaa	ctc	gtc	ctt	tct	aag	cca	tca	gac	aaa	1681

Tyr 545	Leu	Phe	His	Glu	Lys 550	Lys	Leu	Val	Leu	Ser 555	Lys	Pro	Ser	Asp	Lys 560	
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Lys	Ser	Asp	Asp 20	Arg	Pro	Tyr	Ile	Val 25	Leu	Leu	Pro	Leu	Ile 30	Glu	Gly	
Gln	Phe	Arg 35	Ala	Ser	Leu	Gln	Pro 40	Gly	Val	Asp	Asp	Phe 45	Ile	Asp	Ile	
Cys	Val 50	Glu	Ser	Gly	Ser	Thr 55	Lys	Val	Asn	Glu	Ser 60	Ser	Phe	Arg	Ala	
Ser 65	Leu	Tyr	Met	His	Ala 70	Gly	Asp	Asp	Pro	Phe 75	Thr	Leu	Val	Lys	Asp 80	
Ala	Val	Lys	Val	Ala 85	Arg	His	His	Leu	Gly 90	Thr	Phe	Arg	Leu	Leu 95	Glu	
Glu	Lys	Thr	Pro 100	Pro	Gly	Ile	Val	Asp 105	Lys	Phe	Gly	Trp	Cys 110	Thr	Trp	
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Gln	Gly 130	Leu	Val	Asp	Gly	Gly 135	Cys	Pro	Pro	Gly	Leu 140	Val	Leu	Ile	Asp	
Asp 145	Gly	Trp	Gln	Ser	Ile 150	Cys	His	Asp	Asn	Asp 155	Ala	Leu	Thr	Thr	Glu 160	
Gly	Met	Gly	Arg	Thr 165	Ser	Ala	Gly	Glu	Gln 170	Met	Pro	Cys	Arg	Leu 175	Ile	
Lys	Phe	Glu	Glu 180	Asn	Tyr	Lys	Phe	Arg 185	Glu	Tyr	Glu	Ser	Pro 190	Asn	Lys	
Thr	Gly	Pro 195	Gly	Pro	Asn	Thr	Gly 200	Met	Gly	Ala	Phe	Ile 205	Arg	Asp	Met	
Lys	Asp 210	Asn	Phe	Lys	Ser	Val 215	Asp	Tyr	Val	Tyr	Val 220	Trp	His	Ala	Leu	

Cys Gly Tyr Trp Gly Gly Leu Arg Pro Asn Val Pro Gly Leu Pro Glu

225	230	235	240
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Glu Asp Leu Ala Va	al Asp Lys Ile	Val Asn Asn Gly Val	Gly Leu Val
260		265	270
Pro Pro Glu Phe Va	al Glu Gln Met	Tyr Glu Gly Leu His	
275	280	285	
Glu Ser Val Gly I	le Asp Gly Val	Lys Val Asp Val Ile	His Leu Leu
290	295	300	
Glu Met Leu Cys G	lu Asp Tyr Gly	Gly Arg Val Asp Leu	Ala Lys Ala
305	310	315	320
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	25	330	335
Gly Val Ile Ala G	ly Leu Glu His	Cys Asn Asp Phe Met 345	Phe Leu Gly 350
Thr Glu Ala Ile Th 355	nr Leu Gly Arg 360	Val Gly Asp Asp Phe 365	
Asp Pro Ser Gly As	sp Pro Asn Gly	Thr Phe Trp Leu Gln	Gly Cys His
370	375	380	
Met Val His Cys Al	la Tyr Asn Ser	Ile Trp Met Gly Asn	Phe Ile His
385	390	395	
	et Phe Gln Ser	Thr His Pro Cys Ala	Glu Phe His
	05	410	415
Ala Ala Ser Arg Al	a Ile Ser Gly	Gly Pro Ile Tyr Val	Ser Asp Ser
420		425	430
Val Gly Lys His As 435	on Phe Glu Leu 440	Leu Arg Ser Leu Val	Leu Pro Asp
Gly Ser Ile Leu An	rg Cys Asp Tyr	Tyr Ala Leu Pro Thr	Arg Asp Cys
450	455	460	
Leu Phe Glu Asp Pi	to Leu His Asn	Gly Lys Thr Met Leu	Lys Ile Trp
465	470	475	480
Asn Tyr Asn Lys Ph	_	Val Gly Thr Phe Asn	Cys Gln Gly
48		490	495
Gly Gly Trp Ser And 500	rg Glu Val Arg	Arg Asn Gln Cys Ala 505	Ala Glu Tyr 510
Ser His Ala Val Se	er Ser Ser Ala	Gly Pro Ser Asp Ile	Glu Trp Lys
515	520	. 525	
Gln Gly Thr Ser Pr	o Ile Asp Val	Asp Gly Val Lys Thr	Phe Ala Leu
530	535	540	
Tyr Leu Phe His Gl	u Lys Lys Leu	Val Leu Ser Lys Pro	Ser Asp Lys
545	550	555	560

Ile Asp Ile Thr Leu Glu Pro Phe Asp Phe Glu Leu Ile Thr Val Ser 565 570 575

Pro Val Lys Thr Leu Ala Asn Cys Thr Val 580 585

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	1> CI	os 2)	(814)	)									
c ca	_		_			-	_	ne Hi	_	-	rg Al	cc atc la Ile l5	49
											gac Asp		97
											cgg Arg		145
											ccg Pro		193
											ttc Phe		241
											ccc Pro 95		289
				_	_						gcc Ala		337
											ggg Gly		385
											gtc Val		433
											ctc Leu		481
											cgc Arg 175		529

atc tcg cat Ile Ser His							
atg ctc aac Met Leu Asn 195							
gct agc ggc Ala Ser Gly 210							
gtg gcg tac Val Ala Tyr 225							
gag gcc gag Glu Ala Glu							
tgg tcg ggg Trp Ser Gly					_	-	814
tgagccggac g	ggccgat	ga ctctg	cgtct ct	gctccctg	ctggcctg	gct cagga	icataa 874
tctaatgttt a	gagetta	cc aggtt	ttaca gc	tctatcag	tttacttt	tg tttt	ctgct 934
cttcgttttt t	aagaatt	at ttcta	ttgtg tg	aattaatg	agtgcttt	cc ttcta	aaaa 993
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Ser Gly Gly	Pro Ile 20	Tyr Val	Ser Asp 25	Ser Val	Gly Gln	His Asp 30	Phe
Ala Leu Leu 35	Arg Arg	Leu Ala	Leu Pro 40	Asp Gly	Thr Val	Leu Arg	Cys
Glu Gly His	Ala Iou	Pro Thr	Arg Asp	Cys Leu	Phe Ala	Asp Pro	Leu
50	Ara bed	55			60	-	

19

Gly Val Val Gly Ala Phe Asn Cys Gln Gly Gly Gly Trp Ser Pro Glu

Ala Arg Arg Asn Lys Cys Phe Ser Glu Phe Ser Val Pro Leu Ala Ala

Arg Ala Ser Pro Ser Asp Val Glu Trp Lys Ser Gly Lys Ala Gly Pro 115 120 125

85

Gly	Val 130	Ser	Val	Lys	Asp	Val 135	Ser	Gln	Phe	Ala	Val 140	Tyr	Ala	Val	Glu	
Ala 1 145	Arg	Thr	Leu	Gln	Leu 150	Leu	Arg	Pro	Asp	Glu 155	Gly	Val	Asp	Leu	Thr 160	
Leu (	Gln	Pro	Phe	Thr 165	Tyr	Glu	Leu	Phe	Val 170	Val	Ala	Pro	Val	Arg 175	Val	
Ile	Ser	His	Glu 180	Arg	Ala	Ile	Lys	Phe 185	Ala	Pro	Ile	Gly	Leu 190	Ala	Asn	
Met :	Leu	Asn 195	Thr	Ala	Gly	Ala	Val 200	Gln	Ala	Phe	Glu	Ala 205	Lys	Lys	Asp	
Ala	Ser 210	Gly	Val	Thr	Ala	Glu 215	Val	Phe	Val	Lys	Gly 220	Ala	Gly	Glu	Leu	
Val 2 225	Ala	Tyr	Ser	Ser	Ala 230	Thr	Pro	Arg	Leu	Cys 235	Lys	Val	Asn	Gly	Asp 240	
Glu i	Ala	Glu	Phe	Thr 245	Tyr	Lys	Asp	Gly	Val 250	Val	Thr	Val	Asp	Val 255	Pro	
Trp :	Ser	Gly	Ser 260	Ser	Ser	Lys	Leu	Cys 265	Cys	Val	Gln	Tyr	Val 270	Tyr		
<210: <211: <212: <213: - <220: <223:	> 30 > DN > Ar > De	IA tifi scri	.ptic		Art	ific		Sequ	ience	e:syr	nthet	cic				
<4002 aatti	_	ag c	atag	jccaa	ıg tt	aaco	cacct	:								30
<2102 <2112 <2122 <2132	> 24 > DN	ΙA	.cial	. Sec	luenc	e										
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<2103 <2113 <2123 <2133	> 22 > DN	i IA	cial	. Seç	luenc	:e										
<220	>															

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<210><211><211><212><213>	24		
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<400> acaaca	13 agaaa aatatgactc ttattact		28
<220>	26	Sequence: synthetic	
<400> aaaaga	14 agagt caaacatcat agtatc		26
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<220> <223>	Description of Artificial primer 1 (from list 2)	Sequence:synthetic	
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<210>			

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<220>	
<223> Description of Artificial Sequence:synthesis primer 2 (from list 2)	netic
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atggcaccac caagcataac caaaactgca accetecaag ac	ca 43
and the state of t	
·	
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<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
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primer 3 (from list 2)	
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tcaaaataaa aactggacca aagac	25
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<211> 30	•
<212> DNA	
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primer 4 (from fist 2)	
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	•
<210> 19	
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primer 5 (from list 2)	•
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<211> 32	
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<220>	·
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<pre>primer 6 (from list 2)</pre>	
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arygotocaa goataaycaa aactytyyaa ct	32

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<223> Description of Artificial Sequence:synthetic
      primer 7 (from list 2)
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                                                                    25
tcaaaataaa aactcaacca ttgac
<210> 22
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<212> DNA
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      primer 8 (from list 2)
<400> 22
                                                                    39
tcaaaataaa aactcaacca ttgacaattt tgaagcact
<210> 23
<211> 20
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<213> Vicia faba
<400> 23
Gly Ile Lys Phe Met Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr
His Trp Val Gly
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<213> Vicia faba
Ile Ile Asp Lys Phe Gly Trp Cys Thr Trp Asp Ala Phe Tyr
<210> 25
<211> 15
<212> PRT
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Gly Gly Cys Pro Pro Gly Phe Val Ile Ile Asp Asp Gly Trp Gln
                                   · 10
                 5
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<210> 26
<211> 17
<212> PRT
<213> Vicia faba
<400> 26
Thr Ser Ala Gly Glu Gln Met Pro Cys Arg Leu Val Lys Tyr Glu Glu
                                      10
Asn
<210> 27
<211> 16
<212> PRT
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Val Tyr Val Trp His Ala Leu Cys Gly Tyr Trp Gly Gly Val Arg Pro
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<211> 20
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Thr Met Glu Asp Leu Ala Val Asp Lys Ile Val Glu Asn Gly Val Gly
Leu Val Pro Pro
             20
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<211> 23
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Gly Leu His Ser His Leu Glu Ser Ala Gly Ile Asp Gly Val Lys Val
Asp Val Ile His Leu Leu Glu
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<211> 14
<212> PRT
<213> Vicia faba
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Gly Gly Arg Val Glu Leu Ala Arg Ala Tyr Tyr Lys Ala Leu
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Lys Thr Met Leu Lys Ile Trp Asn 20

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<211> 13
<212> PRT
<213> Vicia faba
<400> 36
Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Grp
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<213> Vicia faba
<400> 37
Phe Ala Pro Ile Gly Leu Val Asn Met
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<211> 32
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<221> modified base
<222> (1)..(32)
\langle 223 \rangle n = inosine
<220>
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      primer 1-F (from list 4)
<400> 38
ttnaangtnt ggtggacnac ncantgggtn gg
                                                                     32
<210> 39
<211> 41
<212> DNA
<213> Artificial Sequence
<220>
<221> modified_base
<222> (1)..(41)
<223> n = inosine
<220>
<223> Description of Artificial Sequence:synthetic
      primer 2-F (from list 4)
<400> 39
atnatngana anttnggntg gtgnacntgg gangenttnt a
                                                                     41
<210> 40
<211> 41
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<212> DNA

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<213> Artificial Sequence
<220>
<221> modified base
<222> (1)..(41)
<223> n = inosine
<220>
<223> Description of Artificial Sequence:synthetic
      primer 2-RV (from list 4)
<400> 40
tanaangent eccangtnea ecancenaan tintenatna t
                                                                      41
<210> 41
<211> 44
<212> DNA
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<221> modified base
<222> (1)..(44)
\langle 223 \rangle n = inosine
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      primer 3-F (from list 4)
<400> 41
ggnggntgnc cnccnggntt ngtnatnatn ganganggnt ggca
                                                                      44
<210> 42
<211> 44
<212> DNA
<213> Artificial Sequence
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<221> modified base
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\langle 223 \rangle n = inosine
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      primer 3-RV (from list 4)
<400> 42
tgccancent entenatnat nacnaancen ggnggneane ence
                                                                      44
<210> 43
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<221> modified_base
<222> (1)..(32)
<223> n = inosine
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<220> <223>	Description of Artificial Sequence:synthetic primer 4-F (from list 4)	
<400> aanaar	43 ncant tnaanggnaa nggngtnatn gc	32
<210><211><211><212><213>	32	
<222>	<pre>modified_base (1)(32) n = inosine</pre>	
<220> <223>	Description of Artificial Sequence:synthetic primer 4-RV (from list 4)	
<400> gcnatr	44 nacnc cnttnccntt naantgnttn tt	32
<210><211><212><212><213>	38	
<222>	<pre>modified_base (1)(38) n = inosine</pre>	
<220> <223>	Description of Artificial Sequence:synthetic primer 5-F (from list 4)	
<400> tggatg	45 ggna anttnatnca nccngantgg ganatgtt	38
<210> <211> <212> <213>	38	
<222>	<pre>modified_base (1)(38) n = inosine</pre>	
	Description of Artificial Sequence:synthetic primer 5-RV (from list 4)	
<400> aacatn	·	38

<210> <211> <212> <213>	27		
<222>	<pre>modified_base (1)(27) n = inosine</pre>		
<220> <223>	Description of Artificial primer 6-RV (from list 4)	Sequence:synthetic	
<400> catnt	47 tnacn arncenatng gngenaa		27
<210><211><211><212><213>	26		
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<400> aaracı	48 ngcnc cnagyathat hgacaa	· .	26
<210><211><211><212><213>	20		
<220> <223>	Description of Artificial primer 13.4 (from list 5)	Sequence: synthetic.	
<400> aaratl	49 ntgga ayctnaacaa		20
<210><211><211><212><213>	24		
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<400> aargcı	50 nagrg tngtngtncc naag		24
<210> <211> <212>	21		

<213>	Artificial Sequence	
<220> <223>	Description of Artificial Sequence:synthetic primer 13.3RV (from list 5)	
<400> yttrt		21
<210><211><211><212><213>	21	
<220>	Description of Artificial Sequence:synthetic primer 10.3RV (from list 5)	
<400> yttrt	52 cytor tanagraatt t	21
<210><211><211><212><213>	30	
<220> <223>	Description of Artificial Sequence:synthetic primer RES-2RV (from list 6)	
<400> ggctga	53 aggtt cggttcattc ctgaatcatc	30
<210><211><211><212><213>	30	
<220> <223>	Description of Artificial Sequence:synthetic primer RS-7 (from list 6)	
<400> ccaaat	54 Eggta catattggct ccaaggttgt	30
<210><211><211><212><213>	30	
<220> <223>	Description of Artificial Sequence:synthetic primer RS-8 (from list 6)	
<400> aagagt	55 gtat ctgaattttc acgcgcggtg	30

<210><211>		
<212>		
	Artificial Sequence	
<220s		
<220> <223>	Description of Artificial Sequence:synthetic primer RS-9 (from list 6)	
<400>	56	
tggtg	caatg ggaaaactcc aatgagcacc	30
<210>	57	
<211>	30	
<212>		
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<220>		
<223>	Description of Artificial Sequence:synthetic primer RS-10 (from list 6)	
<400>	57	
	gtgtt ctgatagatt gaaagtttcg	30
<210>	58	
<211>		
<212>		
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<220>		
	Description of Artificial Sequence:synthetic	
	primer RS-11 (from list 6)	
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	ctgg agtttgatga taatgcaagt	30
,		
٠٥١٥٠	50	
<210> <211>		
<211>		
	Artificial Sequence	
	•	
<220>		
<223>	Description of Artificial Sequence:synthetic primer RS-N (from list 7)	
	primer RS-N (from fist /)	
<400>	59	
cgcgga	atcca ccatggcacc accaagcata accaaaactg c	41
<210>	60	
<211>		
<212>	DNA	
<213>	Artificial Sequence	
<220>		
	Description of Artificial Sequence:synthetic	
	primer RS-C (from list 7)	

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tgctctagat tatcaaaata aaaactggac caaagac
<210> 61
<211> 35
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<223> Description of Artificial Sequence:synthetic
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<220>
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<222> (1)..(35)
<223> n= inosine
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cgattnaang tntggtggac nacncantgg gtngg
                                                                       35
<210> 62
<211> 45
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<222> (1)..(45)
\langle 223 \rangle n = inosine
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                                                                       45
ggcctanaan gcntcccang tncaccancc naanttntcn atnat
<210> 63
<211> 41
<212> DNA
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<220>
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<222> (1)..(41)
\langle 223 \rangle n = inosine
<400> 63
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cgatgg	gatgg gnaanttnat ncancengan tggganatgt t	41
<210><211><211><212><213>	32	
	Description of Artificial Sequence:synthetic primer 6-RV (from list 8)	
<222>	<pre>modified_base (1)(32) n = inosine</pre>	
<400> ggccac	64 atnt tnacnarncc natnggngcn aa	32
<210><211><211><212><212><213>	30	
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<400> cacgaa		30
<210><211><212><212><213>	30	
	Description of Artificial Sequence:synthetic primer SC-3RV (from list 9)	
<400> aagcaa		30
<210><211><211><212><213>	30	
	Description of Artificial Sequence:synthetic primer SC-5 (from list 9)	
<400> acacga		30
<210S	68	

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<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:synthetic
      primer SC-6 (from list 9)
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                                                                     25
tggaatctca acaaatatac aggtg
<210> 69
<211> 30
<212> DNA
<213> Artificial Sequence
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      primer SN-3RV (from list 9)
<400> 69
gggtcatggc caacgtggac gtataagcac
                                                                     30
<210> 70
<211> 30
<212> DNA
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<223> Description of Artificial Sequence:synthetic
      primer SN-4RV (from list 9)
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gatgatcact ggcgcggttt tctcctcgag
<210> 71
<211> 35
<212> DNA
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<223> Description of Artificial Sequence:synthetic
      primer 1-F (from list 10)
<220>
<221> modified base
<222> (1)..(35)
\langle 223 \rangle n = inosine
<400> 71
cgattnaang tntggtggac nacncantgg gtngg
                                                                     35
<210> 72
<211> 37
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:synthetic
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<220>
<221> modified base
<222> (1)..(37)
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<400> 72
                                                                      37
ggccagcnat nacncenttn centtnaant gnttntt
<210> 73
<211> 44
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence:synthetic
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<220>
<221> modified base
<222> (1)..(44)
<223> n = inosine
<400> 73
                                                                      44
cgaatnatng anaanttngg ntggtgnacn tgggangcnt tnta
<210> 74
<211> 32
<212> DNA
<213> Artificial Sequence
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\langle 223 \rangle n = inosine
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                                                                      32
ggccacatnt tnacnarnce natnggngen aa
<210> 75
<211> 41
<212> DNA
<213> Artificial Sequence
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      primer 5-F (from list 11)
<220>
<221> modified base
<222> (1)..(41)
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<223> n= inosine	
<400> 75 cgatggatgg gnaanttnat ncancengan tggganatgt t	41
<210> 76 <211> 32 <212> DNA <213> Artificial Sequence	
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<220> <221> modified_base <222> (1)(32) <223> n = inosine	
<400> 76 ggccacatnt tnacnarnce natnggngen aa	32
<210> 77 <211> 25 <212> DNA <213> Artificial Sequence	
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<400> 77 gacgtcgagt ggaagagcgg caagg	25
<210> 78 <211> 25 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:synthetic primer M-11 (from list 12)	
<400> 78 cacctacgag ctcttcgtcg ttgcc	25
<210> 79 <211> 25 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:synthetic primer BamSac-(+) (from list 13)	
<400> 79 gatcgagctc gtgtcggatc cagct	25

<510>	80	
<211>	17	
<212>	DNA	
<213>	Artificial Sequence	
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	primer BamSac-(-) (from list 13)	
<400>	80	
	gaca cgagctc	17
ggaco	gada dgagded	
	•	
<210>	91	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence:synthetic	
	primer 35S (from list 14)	
<400>	81	
ttccag	tatg gacgattcaa ggcttgcttc	30
	·	
<210>	82	
<211>	25	
<212>	DNA	
	Artificial Sequence	
<220>		
	Description of Artificial Sequence:synthetic	
\2237	primer NOS (from list 14)	
	primer NOS (ITOM ITSC 14)	
<100>	00	
<400>		25
atgtat	aatt gcgggactct aatca	25
<210>		
<211>	30	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence:synthetic	
	primer RS-F (from list 14)	
<400>	83	
	gtat ctgaattttc acgcgcggtg	30
aagagt	gear organization adjugacyty	50
<210>	9.4	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence:synthetic	

## primer RS-RV (from list 14)

<400> accttc	84 ccat acaccttttg gatgaacctt caa	33
<210> <211> <212> <213>	38	
	Description of Artificial Sequence:BamHI-NcoI linker (from Fig. 1)	
<400> ggatcc	85 acca tggcaccacc aagcataacc aaaactgc	38
<210> <211> <212> <213>	36	
	Description of Artificial Sequence:XbaI-NotI-SacI linker (from Fig. 1)	
<400> tgataa	86 teta gageggeege caeegeggtg gagete	36
<210> <211> <212> <213>	34	
	Description of Artificial Sequence:XbaI-NotI-SacI linker (from Fig. 1)	
<400> tctaga	87 ttat caaaataaaa actggaccaa agac	34